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atgaggggccctgctcagattttggattcttggtcaggagacgttgt
1 -----
tactcccggggacgagtctaaaaacctaagaaccaggcctctgcaaca
ACTAGTCGACATGAGGGCCCCTGCTCAGTTTGGCTTGTG-3'
A A C AA
MKV4 PRIMER

agaaaatgagaccgtctattcagttcctggggctcttgttctggcttcatgg
49 -----
tctttactctggcagataagtcaaggaccccgagaacaacaagaccgaagtacc

[M - R P S I Q F L G L L L F W L H G
LEADER

tgcctcagtgtgacatccagatgacacagtctccatcctcactgtctgcacatctct
103 -----
acgagtcacactgttaggtctactgtgtcagaggttaggagtgacagacgttagaga

A Q C] [D I Q M T Q S P S S L S A S L
FR1
gggaggcaaagt caccatcacttgcaagacaagccaagacattaacaagtatat
157 -----
ccctccgtttcagtggtagtgaacgttctgttcggttctgtaattgttcatata

G G K V T I T C] [K T S Q D I N K Y M
CDR1

ggcttggtaccaacacaaggcctggaaaacgtcctaggctgctcatacattacac
211 -----
ccgaaccatggtgtgttcggacctttgcaggatccgacgagtatgtaatgtg

A] [W Y Q H K P G K R P R L L I H] [Y T
FR2

atctgcattacagccaggcatccatcaagggtcagtgaaagtgggtctggag
265 -----
tagacgtaatgtcggtccgtagggtagttccaagtcacccttcacccagaccctc

S A L Q P] [G I P S R F S G S G S G R
CDR2

FIG. 1-1.

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agattattccttcaacatcagcaacacctggaggcctgaagatattgcaacttatta
319 -----
tctaataaggaagttagtcgttgacctcgacttctataacgttgaataat

D Y S F N I S N L E P E D I A T Y Y
FR3

ttgtctacagtatgataatctgtggacgttcgggtggaggcaccaagctggaaat
373 -----
aacagatgtcatactattagacacacctgcaagccacccgtgggtcgaccttta

C] [L Q Y D N L W T] [F G G G T K L E I
CDR3 FR4

MOUSE KAPPA PRIMER
3' - GTAGAAGGGTGGTAGGTGGGCCCT
caaacgggctgatgctgcaccaactgttatccatcttcccaccatccacccggga
427 -----
gtttgcccgactacgacgtggttgacataggtagaagggtggtaggtggccct

K]

AGG-5'
tcc
481 ---
agg

FIG. 1-2.

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1 atgaaatgcagctgggtcatgttcttcgtggcagtggttacaggg
 1 -----
 tactttacgtcgaccaggtaacaagaaggactaccgtcaccaatgtccc
 ACTAGTCGACATGAAATGCAGCTGGGTCACTTCTTC-3'
 G

MHV1 PRIMER
 [M K C S W V M F F L M A V V T G
 LEADER

49 gtcaattcagagggttcagctgcagcagtctggggcagagcttgtgaagccaggg
 49 -----
 cagtttaagtctccaagtcgacgtcgtagacccgtctcgaacacttcggtccc
 V N S] [E V Q L Q Q S G A E L V K P G
 FR1

103 gcctcagtcaagttgtcctgcacagcttctggcttcaacattaaagacacccat
 103 -----
 cggagtcagttcaacaggacgtgtcgaagaccgaagttgttaattctgtggata
 A S V K L S C T A S G F N I K] [D T Y
 CDR1

157 atacactgtgtgaagcagaggcctgaacagggcctggagtggatttggaggatt
 157 -----
 tatgtgacacacttcgtctccggacttgcacccggacctcacctaaccctcctaa
 I H] [C V K Q R P E Q G L E W I G] [R I
 FR2

211 gatcctgcgaatggttataactaaatatgaccgaagttccagggcaaggccact
 211 -----
 cttaggacgcttaccaatatgatttatactgggcttcaggtcccggtccgggtga
 D P A N G Y T K Y D P K F Q G] [K A T
 CDR2

265 ataacagctgacacatcctccaacacacaggctacctgcagctcagcagcctgaca
 265 -----
 tattgtcgactgtgttaggagggtgtgtcggtggacgtcgagtcgtcgactgt
 I T A D T S S N T A Y L Q L S S L T
 FR3

FIG. 2-1.

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tctgaggacactgccgtctatttctgtgctagagagggatattatggtaactac
319 -----
agactcctgtgacggcagataaagacacacgtctccctataataccattgatg

S E D T A V Y F C A R] [E G Y Y G N Y
CDR3

ggggtctatgctatggactactggggtcaaggaacctcagtccccgtctcctca
373 -----
ccccagatacgatacctgatgaccccagttccttggagtcaagtggcagaggagt

G V Y A M D Y] [W G Q C T S V T V S S]

MOUSE GAMMA-1 PRIMER

3' -GTAGACAGATAGGTGACCGGGGCCCTAGG-5
gc当地aaacgacaccccatctgtctatccactggcccccggatcc
427 -----
cggtttgctgtggggtagacagataggtgaccggggccctagg

S S]

FIG. 2-2.

HindIII KOZAK SEQUENCE

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aagcttgccgcaccatgagaccgtctattcagttcctgggctttgttggc
 1 -----
 ttcgaacggcggtggtactctggcagataagtcaaggacccgagaacaacaag

[M R P S I Q F L G L L L F
 LEADER

tggcttcatggtgctcagtgtgacatccagatgacacagtctccatcctcactg
 55 -----
 accgaagtaccacgagtcacactgttaggtctactgtgtcagaggtaggagtgac

W L H G A Q C] [D I Q M T Q S P S S L
 FR1

tctgcatctGTAgaGATAGAgtcaccatcacttgcaagacaagccaagacatt
 109 -----
 agacgtagaCATcctCTATCTcagtggtagtgaacgttctgtcggtctgtaa

S A S V G D R V T I T C] [K T S Q D I
 CDR1

aacaagtatatggcttggtagccaaCAGACAcctggaaaaGCTcctaggctgctc
 163 -----
 ttgttcatataaccgaaccatggttGTCTGTggacctttCGAggatccgacgag

N K Y M A] [W Y Q Q T P G K A P R L L
 FR2

atacattacacatctgcattacagccaggcatcccataaggtagtggaaatg
 217 -----
 tatgtaatgttagacgtaatgtcggtccgttaggtagttccaaatcacattca

I H] [Y T S A L Q P] [G I P S R F S G S
 CDR2

gggtctggagagattatACTttcACCatcagcAGCctgCAGcctgaagatatt
 271 -----
 cccagaccctcttaataTGAAagTGGtagtcgTCGgacGTCggacttctataa

G S F R D Y T F T I S S L Q P E D I
 FR3

FIG. 10-1.

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325 gcaacttattattgtctacagtatgataatctgtggacgttcggtCAAggcacc

cgttgaataataaacagatgtcatactattagacacacctgcaagccaGTTccgtgg

A T Y Y C] [L Q Y D N L W T] [F G Q G T
CDR3 FR4

SPLICE DONOR SITE BamHI
aagGTGaaatcaaacgtgagtggtggatcc
379 -----
ttcCACcttagttgcactcacctagg

K V E I K]

FIG. 10-2.

HindIII KOZAK SEQUENCE
AAGCTTGCCGCCACCATGGACTGGACCTGGCGCGTTTTGCGCTGCTCGCCGTG
1 -----
TTCGAACGGCGGTGGTACCTGACCTGGACCGCGCACAAAACGGACGAGCGGCAC

[M D W T W R V F C L L A V
LEADER

GCTCCTGGGGCCCACAGCCAGGTGCAACTAGTGCAGTCCGGCGCCGAAGTGAAG
55 -----
CGAGGACCCCGGGTGTGGTCCACGTTGATCACGTCAAGGCCGGCTTCACCTC

A P G A H S] [Q V Q L V Q S G A E V K

AAACCCGGTGCTTCCGTGAAAGTCAGCTGTAAAGCTAGCGGTttcaacattaaa
109 -----
TTTGGGCCACGAAGGCACTTCAGTCGACATTGATCGATGCCAagttgttaattt

K P G A S V K V S C K A S G F N I K] [
FR1

gacacctataatacactGGGTTAGACAGGCCCTGGCCAAaGGCTgGAGTGGATg
163 -----
ctgtggatatatgtgACCCAATCTGTCCGGgGaCCGGTTtCCGAcCTCACCTAc

D T Y I H] [W V R Q A P G Q R L E W M
CDR1 FR2

FIG. 11-1.

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217 GGaaggattgatcctgcgaatggttatactaaatatgaccgcgaagttccaggcg

 CCttcctaacttaggacgcttaccaatatgatttatactgggcttcaaggcccgc
 G] [R I D P A N G Y T K Y D P K F Q G] [
 CDR2

271 cgggtcACCCatcACCgcaGACACCTCTgccagcACCGCCTACATGGAACTGTCC

 gcccagTGGtagTGGcgtCTGTGGAGAcggtcgTGGCGGATGTACCTTGACAGG
 R V T I T A D T S A S T A Y M E L S
 FR3

325 AGCCTGCGCTCCGAGGACACTGCAGTCTACTACTGCGCCagagagggatattat

 TCGGACGCGAGGCTCCTGTGACGTCAGATGATGACGCGGtctctccctataata
 S L R S E D T A V Y Y C A R] [E G Y Y
 379 ggtaactacgggtctatgctatgACTAcTGGGGtCAaGGaACCCTTGTCAACC

 ccattgatccccagatacgatacCTGATgACCCaGTtCCtTGGGAACAGTGG
 G N Y G V Y A M D Y] [W G Q G T L V T
 CDR3 FR4

SPLICE DONOR SITE BamHI
 433 GTCcCTCAGGTGAGTGGATCC

 CAGaggAGTCCACTCACCTAGG
 V S S]

FIG. 11-2.